IFWO

RAW SEQUENCE LISTING   DATE: 08/20/2004
PATENT APPLICATION: US/10/764,330   TIME: 10:46:02

Input Set : A:\SEQ.Listing.ST25.txt.txt
Output Set: N:\CRF4\08202004\J764330.raw

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 3 <110> APPLICANT: Cooke, Michael P.
 4         Sauer, Karsten
 5         Wiltshire, Tim
 6         Tarantino, Lisa
 7         Fletcher, Colin
 8         Wen, Ben
10 <120> TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING T LYMPHOCYTES
12 <130> FILE REFERENCE: P1097US10
14 <140> CURRENT APPLICATION NUMBER: US 10/764,330
15 <141> CURRENT FILING DATE: 2004-01-23
17 <150> PRIOR APPLICATION NUMBER: US 60/442,792
18 <151> PRIOR FILING DATE: 2003-01-25
20 <160> NUMBER OF SEQ ID NOS: 4
22 <170> SOFTWARE: PatentIn version 3.2
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 1192
26 <212> TYPE: PRT
27 <213> ORGANISM: Mus musculus
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36              20                  25                  30
39 Phe Ala Leu Cys Pro Pro Pro Arg Pro Cys Cys Ser Ile Ser Ala Gln
40          35                  40                  45
43 Ser Tyr Gly Arg Arg Ala Ser Gly Thr Lys Pro Arg Ala Ala Gly Gly
44      50                  55                  60
47 Gly Gly Ala Gly Gly Gly Ala Gly Arg Arg Ala Ala Ala Ala Gly Gly
48 65                  70                  75                  80
51 Pro Cys Thr Met Ala Val Tyr Cys Tyr Ala Leu Asn Ser Leu Val Ile
52              85                  90                  95
55 Met Asn Ser Thr Asn Glu Leu Lys Ser Gly Gly Pro Arg Pro Ser Gly
56              100                 105                 110
59 Ser Glu Thr Pro Gln Pro Ser Gly Arg Ala Ala Leu Ser Pro Gly Ser
60              115                 120                 125
63 Val Phe Ser Pro Gly Arg Gly Ala Ser Phe Leu Phe Pro Pro Ala Glu
64      130                 135                 140
67 Ser Leu Ser Leu Glu Glu Pro Gly Ser Pro Gly Gly Trp Arg Ser Gly
68 145                 150                 155                 160
71 Arg Arg Arg Leu Asn Ser Ser Ser Gly Ser Gly Gly Gly Ser Ser Ser
72              165                 170                 175
75 Ser Asn Ser Ser Ser Ser Ser Gly Val Gly Ser Pro Ser Trp Ala Gly
76              180                 185                 190
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 80           195                 200                 205
 83 Pro Pro Gly Pro Glu Glu Ala Gln Arg Lys Leu Arg Ile Leu Gln Arg
 84           210                 215                 220
 87 Glu Leu Gln Asn Val Gln Val Asn Gln Lys Val Gly Met Phe Glu Ala
 88 225                 230                 235                 240
 91 Gln Ile Gln Ala Gln Ser Ser Ala Ile Gln Ala Pro Arg Ser Pro Arg
 92               245                 250                 255
 95 Leu Gly Arg Ala Arg Ser Pro Ser Pro Cys Pro Phe Arg Ser Ser Ser
 96               260                 265                 270
 99 Gln Pro Pro Glu Arg Val Leu Ala Pro Cys Ser Pro Ser Glu Glu Arg
100           275                 280                 285
103 Arg Thr Lys Ser Trp Gly Glu Gln Cys Thr Glu Thr Pro Asp Thr Asn
104           290                 295                 300
107 Ser Gly Arg Arg Ser Arg Leu Ser Thr His Pro Ser Lys Asp Lys Glu
108 305                 310                 315                 320
111 Gly Val Ala Pro Leu Leu Gly Pro Ala Ser Pro Thr Arg Leu Gly Thr
112               325                 330                 335
115 Gln Ser Pro Ser Thr Ser Val Arg Met Glu Arg Gly Thr Pro Ala Ser
116               340                 345                 350
119 Pro Arg Cys Gly Ser Pro Thr Pro Met Glu Thr Asp Lys Arg Val Ala
120               355                 360                 365
123 Pro Ser Leu Glu Arg Phe Gly Thr Ser Leu Thr Leu Ala Thr Lys Val
124           370                 375                 380
127 Ala Ala Ser Ala Ala Ser Ala Gly Pro His Pro Gly His Asp Ser Ala
128 385                 390                 395                 400
131 Leu Met Glu Thr Gly Cys Glu Leu Gly Gly Met Arg Pro Trp Glu Ala
132               405                 410                 415
135 Gln Met Glu Arg Arg Gly Gln Phe Leu Gly Lys Glu Thr Gly Ser Thr
136               420                 425                 430
139 Pro Glu Pro Val Arg Thr His Met Arg Glu Pro Pro Gly Arg Val Gly
140           435                 440                 445
143 Arg Gly Ile His Ser Val Gly Gly Gln Gly Ser Trp Thr Pro Glu Val
144           450                 455                 460
147 Ile Lys Arg Pro Glu Glu Arg Ala Val Thr Ala Gln Ser Ser Glu Pro
148 465                 470                 475                 480
151 Ser Glu Asp Pro Arg Trp Ser Arg Leu Pro Val Asp Leu Asp Ser Val
152               485                 490                 495
155 Gly Pro Glu Lys Gly Gly Asn Arg Ile Pro Gly Met Arg Gly Pro Gln
156           500                 505                 510
159 Gln Thr Leu Asp Ser Glu Arg Glu Gly Ser Pro Ala Leu Gly Leu Leu
160           515                 520                 525
163 Gly Gly Ser Gln Ala Ala Gln Pro Gly Ala Arg Gly Val Glu Glu Asp
164           530                 535                 540
167 Val His Tyr Gly Arg Met Leu Glu Pro Leu Pro Pro Gly Glu Val Thr
168 545                 550                 555                 560
171 Thr Lys Leu Lys Glu Pro Gln Cys Leu Pro Gly Asp Arg Met Gly Met
172               565                 570                 575
175 Gln Pro Glu Ser Ser Ile Val Trp Pro Ser Ala Leu Glu Glu Ala Pro
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179 Leu Ile Trp Thr Arg Asp Thr Gly Val Gln Ser Lys Gly Thr Trp Gly
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183 Ser Gln Leu Pro Asp Gly Asp Ala His Pro Ser Cys Gln Glu Met Pro
184     610             615             620
187 Pro Asp Gln Lys Asp Lys Ala Ser Leu Lys Glu Ala Cys Ser Pro Ser
188 625             630             635             ' 640
191 Asn Ile Pro Ala Ile Pro Ala Val Ile Ile Thr Asp Met Gly Ala Gln
192             645             650             655
195 Glu Asp Gly Gly Leu Glu Glu Ile Gln Gly Ser Pro Arg Gly Pro Leu
196         660             665             670
199 Pro Leu Arg Lys Leu Ser Ser Ser Ser Ala Ser Ser Thr Gly Phe Ser
200         675             680             685
203 Ser Ser Tyr Asp Asp Ser Glu Glu Asp Ile Ser Ser Asp Pro Glu Arg
204     690             695             700
207 Thr Leu Asp Pro Asn Ser Ala Phe Leu His Thr Leu Asp Gln Gln Lys
208 705             710             715             720
211 Pro Arg Val Ser Lys Ser Trp Arg Lys Ile Lys Asn Met Val Gln Trp
212             725             730             735
215 Ser Pro Phe Val Met Ser Phe Lys Lys Lys Tyr Pro Trp Ile Gln Leu
216             740             745             750
219 Ala Gly His Ala Gly Ser Phe Lys Ala Ala Ala Asn Gly Arg Ile Leu
220         755             760             765
223 Lys Lys His Cys Glu Ser Glu Gln Arg Cys Leu Asp Arg Leu Met Ala
224     770             775             780
227 Asp Val Leu Arg Pro Phe Val Pro Ala Tyr His Gly Asp Val Val Lys
228 785             790             795             800
231 Asp Gly Glu Arg Tyr Asn Gln Met Asp Asp Leu Leu Ala Asp Phe Asp
232             805             810             815
235 Ser Pro Cys Val Met Asp Cys Lys Met Gly Val Arg Thr Tyr Leu Glu
236             820             825             830
239 Glu Glu Leu Thr Lys Ala Arg Lys Lys Pro Ser Leu Arg Lys Asp Met
240         835             840             845
243 Tyr Gln Lys Met Val Glu Val Asp Pro Glu Ala Pro Thr Glu Glu Glu
244     850             855             860
247 Lys Ala Gln Arg Ala Val Thr Lys Pro Arg Tyr Met Gln Trp Arg Glu
248 865             870             875             880
251 Thr Ile Ser Ser Thr Ala Thr Leu Gly Phe Arg Ile Glu Gly Ile Lys
252             885             890             895
255 Lys Glu Asp Gly Ser Val Asn Arg Asp Phe Lys Lys Thr Lys Thr Arg
256         900             905             910
259 Glu Gln Val Thr Glu Ala Phe Arg Glu Phe Thr Lys Gly Asn Gln Asn
260         915             920             925
263 Ile Leu Ile Ala Tyr Arg Asp Arg Leu Lys Ala Ile Arg Ala Thr Leu
264     930             935             940
267 Glu Ile Ser Pro Phe Phe Lys Cys His Glu Val Ile Gly Ser Ser Leu
268 945             950             955             960
271 Leu Phe Ile His Asp Lys Lys Glu Gln Ala Lys Val Trp Met Ile Asp
272             965             970             975
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275 Phe Gly Lys Thr Thr Pro Leu Pro Glu Gly Gln Thr Leu Gln His Asp
276              980             985             990
279 Val Pro Trp Gln Glu Gly Asn Arg  Glu Asp Gly Tyr Leu  Ser Gly Leu
280          995             1000             1005
283 Asp Asn  Leu Ile Asp Ile Leu  Thr Glu Met Ser Gln  Gly Ser Pro
284      1010             1015             1020
287 Leu Thr  Gly His Arg His Arg  Ala Pro Cys His Phe  Ala Arg His
288      1025             1030             1035
291 Leu Cys  Leu Ser Pro Leu Ser  Ser Pro Asn Ser Ser  Phe Ser Cys
292      1040             1045             1050
295 Leu Ser  Ala Tyr Leu Glu Gln  Ser Leu Pro Ser Ala  Leu Gln Asp
296      1055             1060             1065
299 Thr Leu  Glu Lys Lys Lys Arg  Phe Phe Phe Ser Arg  Ser Leu Leu
300      1070             1075             1080
303 Pro Arg  Pro Pro Thr Gly Leu  Gly Gly Gly Val Ser  His Ala Leu
304      1085             1090             1095
307 Ile Glu  Pro Pro Ser Arg Arg  Glu Leu His Lys Ala  Arg Pro His
308      1100             1105             1110
311 Ile Leu  Leu His Ser Glu Ser  Ala Arg Val Gln Lys  Ala Val Ser
312      1115             1120             1125
315 Leu Val  Ala Ser Leu Glu Arg  Leu Ser Leu Pro Leu  Gly Asp Thr
316      1130             1135             1140
319 Ala Pro  Leu Pro Glu Asn Ser  Gly Pro His Trp Leu  Pro Val Gly
320      1145             1150             1155
323 Ala Leu  Leu Pro Pro Ser Gly  Cys His Gln Ala Gln  Ser His Leu
324      1160             1165             1170
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345 gtgctgagcc ccggcagcgt tttcagcccc gggagaggcg cctctttcct cttccccca       180
347 gccgagtcgc tgtcccccga ggagccccgg agccccgggg gctggcggag cggccggcgc      240
349 aggctgaata gtagcagcgg cagtggcagc ggcagcagcg gcagtagcgt gagcagccca      300
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353 ccgccagggc cggaggaggc caagaggaag ctgcggatct tgcagcgcga gttgcagaac      420
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361 aggacaaagt cctgggggga gcaatgtcca gagacttcag gaaccgactc cgggaggaaa      660
363 ggagggccca gcctatgctc ctcgcaggtg aagaaaggaa tgccacctct tcccggccgg      720
365 gctgccccta caggatcaga ggctcaggt ccatccgctt ttgtaaggat ggagaagggt       780
367 atccctgcca gtcccgctg tggctcaccc acagctatgg aaattgacaa aaggggctct       840
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373 cttgccctca ctgagccgtc tgggagagcc cgtgagcttg aggacctgca gcccccagag       1020
375 gccctggtgg agaggcaggg gcagtttctg ggcagtgaga caagcccagc cccagaaagg       1080
377 ggcgggcccc gcgatggaga accccctggg aagatgggga aaggatatct gccctgtggc       1140
379 atgccgggct ctggggagcc tgaagtgggc aaaaggccag aggagacgac tgtgagcgtg       1200
381 caaagcgcag agtcctctga tgccctgagc tggtccaggc tgcccaggggc cctggcctcc      1260
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387 ccggggaccg ggaatgtgga ggcgggaatt ccttctggca gaatgctgga gcctttgccc       1440
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405 aaacctagag tgagcaaatc atggaggaag ataaaaaaca tggtgcactg gtctcccttc       1980
407 gtcatgtcct tcaagaagaa gtacccctgg atccagctgg caggacacgc agggagtttc       2040
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415 gtgatggact gcaagatggg aatcaggacc tacctggagg aggagctcac gaaggcccgg       2280
417 aagaagccca gcctgcggaa ggacatgtac cagaagatga tcgaggtgga ccccgaggcc       2340
419 cccaccgagg aggaaaaagc acagcgggct gtgaccaagc cacggtacat gcagtggcgg       2400
421 gagaccatca gctccacggc caccctgggg ttcaggatcg agggaatcaa aaaagaagac       2460
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425 agagagttca ctaaaggaaa ccataacatc ctgatcgcct atcgggaccg gctgaaggcc       2580
427 attcgaacca ctctagaagt ttctcccttc ttcaagtgcc acgaggtcat ggcagctcc        2640
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431 accacgcccc tgcctgaggg ccagaccctg cagcatgacg tccctggca ggaggggaac         2760
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448 ctgagccccg gcagcgtctt cagccctggg agaggcgcct cctttctctt cccccagca        180
450 gagtcgctgt cgctggagga gcctgggagt gctggggggtt ggcgcagcgg ccgacggagg       240
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454 ggcgtgggca gtcccagttg ggctggccgc ctgcgagggg acgcgcagca ggtggtggcg        360
456 acccgcatcc tctccccacc tgggccggag gaggcccaga ggaagctgag gattctgcag        420
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VERIFICATION SUMMARY
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DATE: 08/20/2004
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